SYSTEMATIC RESOLUTION OF THE GENERA OF THE *CRINIA* COMPLEX (AMPHIBIA: ANURA: MYOBATRACHIDAE)

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Abstract.—Re-evaluation of morphological analyses and generic taxonomy of Australian myobatrachine frogs in the Crinia complex is undertaken in light of new genetic data. All species currently in the genera Ranidella and Crinia are assigned to Crinia. The genera Paracrinia and Geocrinia are retained.

Four Australian genera, Ranidella, Crinia, Paracrinia, and Geocrinia (Myobatrachidae: Myobatrachinae), collectively designated the "Crinia complex," comprise a group of small, rather nondescript frogs (Heyer & Liem 1976). The species of this complex have been partitioned into genera by recent authors with differing results. All recent authors agree concerning the smallest groups of species clusters in this complex, but considerable disagreement exists regarding the assignment of these groups at the generic level. Currently hypothesized groups and classifications are summarized in Table 1.

The following morphological and behavioral characters differentiate the species clusters: vomer and vomerine teeth, omohyoideus muscle, outer metatarsal tubercle, belly texture, egg placement, and mating call. However, clustering algorithms provide no unequivocal pattern of relationships among these species: "There is no way to group the . . . taxa so that two of the derived states of these characters define the same assemblage. Rather, a grouping which results in a cluster having all the taxa with the same derived state of one character leads to convergence of states in the other characters" (Heyer and Liem 1976:9). Thus, the data presented by Heyer and Liem (1976) are certainly open to alternate clustering interpretations than theirs. The phenetic analyses of Blake (1973) and Thompson (1981) recognize the same basic species groups, but the clustering pattern of the groups was highly variable dependent on data scoring and the algorithm used. Within the Crinia complex, morphological variation is so limited that it has been impossible to achieve a stable clustering scheme and, hence, taxonomic consensus. For these cases where the nature of the morphological data preclude a definitive analysis of relationships, use of a different data base is required for analysis of relationships.

Daugherty and Maxson (in press) recently estimated genetic relationships among species of the *Crinia* complex based on MC'F (micro-complement fixation) data from the serum protein albumin. These genetic data, in concert with the morphological data, provide a new basis for determining evolutionary lineages within the complex. The major lineages are herein proposed as generic units in order to provide a stable classification for this complex.

The Genetic Data

Immunological distances derived from comparisons of serum albumins provide both cladistic information and a time framework for interpreting evolutionary

	Blake, 1973	Heyer & Liem, 1976	Thompson, 1981	This study	
georgiana	Together with haswelli, Crinia	Crinia	Not studied	Crinia	
haswelli	Together with georgiana, Crinia	Paracrinia	Not studied	Paracrinia	
laevis cluster	Geocrinia	Geocrinia	Not studied	Geocrinia	
signifera cluster	Species group of Ranidella	Ranidella	Distinct species group of Ran-idella	Crinia	
riparia	Together with tasmaniensis, second species group of Ranidella	Together with tasmaniensis, Australocrinia	Second distinct species group of Ranidella	Crinia	
tasmaniensis	Together with ri- paria, second species group of Ranidella	Together with ri- paria, Austral- ocrinia	Third distinct species group of Ranidella	Crinia	

Table 1.—Species clusters and generic assignment of the Crinia complex.

relationships. In the past decade, such protein data have been used extensively in phylogenetic studies of diverse amphibian taxa (e.g., Heyer and Maxson 1982; Maxson 1981). Albumin immunological distances (ID) have been shown to estimate sequence differences in albumins between species (Maxson and Wilson 1974) and to accumulate measurable sequence differences at an approximate rate of one substitution per lineage per million years (Wilson et al. 1977). Daugherty and Maxson (in press) have measured a series of immunological distances among the albumins of many members of the *Crinia* complex. The data consist of one-way comparisons to *signifera*, currently assigned to the genus *Ranidella* (Table 2). The pattern of divergence from *signifera* reveals the major genetic lineages within this complex.

Members of the signifera cluster (Table 2) exhibit ID values ranging from 24 to 40. The distance to riparia is 15 units and to tasmaniensis is 53 units. Clearly, riparia belongs to the same genetic lineage as other members of the signifera cluster. The ID value for tasmaniensis is somewhat higher than values measured to members of the signifera group, but not as large as values to other lineages (haswelli and laevis; see below) within the Crinia complex. Furthermore, an ID value of around 50 is often seen between species within other frog genera (e.g., Maxson and Wilson 1975; Heyer and Maxson 1981). The immunological evidence thus supports Thompson's (1981) proposal that Australocrinia (i.e., riparia and tasmaniensis) be synonymized with Ranidella (i.e., the signifera cluster).

The ID to georgiana is 29 units, suggesting that georgiana is part of the same genetic lineage as the frogs in the signifera cluster. For both georgiana and riparia, the ID values to signifera are smaller than most ID values measured between signifera and other members of the signifera group. The taxonomic

Table 2.—Albumin immunological distances between *signifera* and other species of the *Crinia* complex.*

	Species compared	ID to signifera	
signifera cluster:			
	signifera	0	
	glauerti	24	
	parinsignifera	24	
	bilingua	30	
	sp. nov.	31	
	remota	31	
	deserticola	40	
	riparia	15	
	tasmaniensis	53	
	georgiana	29	
	victoriana	133	
	haswelli	140	

^{*} Data from Daugherty and Maxson (in press).

conclusions are that Ranidella (including Australocrinia) and Crinia are congeneric and that Ranidella is a synonym of Crinia.

On the other hand, the ID value of *signifera* to *victoriana*, the only member of the *laevis* group tested to date, is 133. This very large value is concordant with recognition of the genus *Geocrinia*. The ID of *signifera* to *haswelli* is similarly high, 140. The similar, but high, ID values of *haswelli* and *victoriana* to *signifera* indicate a distant relationship of *haswelli* and *victoriana* to *signifera*. The values do not indicate what the relationship of *haswelli* is to *victoriana*; it could be close or distant. In fact, preliminary data (Maxson and Daugherty, unpublished) indicate a distant relationship between those taxa (ID value between 90 and 100). These data are consistent with recognition of the genera *Geocrinia* (including *victoriana*) and *Paracrinia* (including *haswelli*).

Discussion

Several conclusions regarding evolution of the *Crinia* complex logically follow from recognition of the genera *Crinia*, *Geocrinia*, and *Paracrinia*.

Several of the character states that differentiate among the species clusters have apparently evolved independently several times. Loss of the vomer and vomerine teeth has occurred within both *Crinia* and *Geocrinia*. Both smooth and granular bellied frogs occur in the genus *Crinia*. All major variation in mating call occurs within the genus *Crinia*. Perhaps most notable is that variations in life history occur within, rather than among lineages. The change from a lotic to lentic egg placement and larval morphology has taken place entirely within the genus *Crinia*, and these life history differences cannot be used to define generic units. A similar situation occurs within the genus *Geocrinia*, with evolution of terrestrial larvae from pond larvae.

The morphological characters that differentiate among the genetically defined lineages are, for the most part, characters involving reduction or loss as the derived state. *Crinia* species have an outer metatarsal tubercle; *Geocrinia* species

lack the tubercle. *Crinia* species have an omohyoideus muscle; *Paracrinia* lacks the muscle. *Geocrinia* species lack an outer metatarsal tubercle and toe fringing; *Paracrinia* has a metatarsal tubercle and toe fringing. Of these characters, the only one that does not involve reduction or loss as the derived state is the metatarsal tubercle (Heyer and Liem 1976).

Derived states involving reduction or loss are usually considered to contain little or no phyletic information (Hecht and Edwards 1976). That morphological states of loss or reduction are the primary criteria permitting morphological discrimination of the genera within the *Crinia* complex (which the genetic data show to be greatly differentiated) suggests that the use in systematics of characters of loss and reduction needs re-evaluation. It also further documents the extreme morphological conservatism so often observed in anuran evolution (Maxson and Wilson 1975; Wilson *et al.*, 1977) and reinforces the need to examine genetic and other categories of characters when conducting phylogenetic studies (Blake 1973).

Generic Redefinition

Crinia is the only genus requiring redefinition. The format used is comparable to that of Heyer and Liem (1976), which may be referred to for definitions of the genera *Geocrinia* and *Paracrinia*.

Crinia Tschudi, 1838

Synonyms.—Ranidella Girard, 1853
Camariolus Peters, 1863
Pterophrynus Lutken, 1863
Pterophryne Gunther, 1867
Australocrinia Heyer and Liem, 1976.

Type species.—Crinia georgiana Tschudi, 1838.

Diagnosis.—A myobatrachine genus; cervical cotyles widely separated; vomer and vomerine teeth present or absent; narrow sacral diapophyses; depressor mandibulae muscle with or lacking a slip from the dorsal fascia; omohyoideus muscle present; tympanum present; belly smooth or granular; toes with or without fringe; outer metatarsal tubercle present; eggs placed in water or on land; pond or stream larvae.

Content.—Crinia bilingua, deserticola, georgiana, glauerti, insignifera, parinsignifera, pseudinsignifera, remota, riparia, signifera, perhaps sloanei (see Thompson 1981), subinsignifera, tasmaniensis, tinnula, and undescribed species. Present knowledge of variation within this genus (as here defined) does not support the recognition of species groups (also see Daugherty and Maxson, in press).

Acknowledgments

We thank P. Baverstock and his family for assistance in collecting sufficient C. signifera to produce an antibody. We thank the many other people who provided us with specimens. Portions of this work were carried out at the Institute of Medical and Veterinary Science in Adelaide, Australia. We thank M. Krieg, P. Baverstock, M. Adams, and C. Watts for stimulation and support while in Adelaide. Financial support came in part from NSF grant INT 79-24146 to LRM and NIH grant 1-F32FM06788-01 to CHD.

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